

CLAIM AMENDMENTS

1-31. (canceled)

32. (currently amended): A method of detecting post-transcriptional gene silencing (PTGS) of a target gene in an organism which method comprises the steps of:

~~analyzing-detecting in a~~ nucleic acid extract prepared from said organism in which organism it is suspected that PTGS is occurring ~~to determine~~ the presence [[or]] as opposed to the absence of short RNA molecules (SRMs) which are 20-30 nucleotides in length in said extract,

characterizing any SRMs which are present in said extract ~~to determine sequence- wherein~~ said characterizing comprises determining identity or similarity with said target gene,

wherein the presence of any SRMs having ~~sequence-~~identity or similarity with said target gene indicates silencing of [[the]] said target gene in the organism.

33. (withdrawn): The method of claim 32, wherein the organism is a plant.

34. (withdrawn): The method of claim 32, wherein the organism is a nematode.

35. (previously presented): The method of claim 32, wherein the organism is a mammal.

36. (previously presented): The method of claim 32 wherein the SRMs are short anti-sense RNA molecules (SARMs).

37. (previously presented): The method of claim 32 wherein the SRMs are short sense RNA molecules (SSRMs).

38. (canceled)

39. (previously presented): The method of claim 32, wherein the silencing of said target gene in the organism is associated with pathogen derived resistance.

40. (previously presented): The method of claim 32, wherein the silencing of said target gene in the organism is associated with modification of a specific trait by co-suppression of the target gene.

41. (currently amended): The method of claim 32, wherein the step of characterizing any SRMs present in the extract to determine ~~sequence~~ identity or similarity with a target gene is performed by a process that comprises:

tagging said SRMs with a marker, and
preparing-probing a library of genes from said organism, and
identifying [[those]] the genes in said library which share sequence identity or similarity,
with any SRMs which are present in the extract as being genes which are silenced in the organism
that bind to said SRMs whereby a gene that binds to said SRM is identified as said target gene
which is silenced.

42-48. (canceled)

49. (currently amended): The method of claim 32, wherein said short RNA molecules are 20-25 nucleotides in length.

50-65. (canceled)

66. (new): The method of claim 32 wherein said determining identity or similarity comprises determining sequence identity or similarity.